

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 13:01:31 ; Search time 13.3043 seconds
(without alignments)
112.230 Million cell updates/sec

Title: US-09-801-784A-1

Perfect score: 173
Sequence: 1 VEKNITVTASVDPITDILQADGSLPSAVALTSPDA 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 112892

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 155 | 89.6 | 170 | 1 FMC1_ECOLI | P02871 escherichia |
| 2 | 153 | 88.4 | 171 | 1 FMS1_ECOLI | P25730 escherichia |
| 3 | 60.5 | 35.0 | 714 | 1 YFE1_YEAST | P43556 saccharomyc |
| 4 | 58 | 33.5 | 1051 | 1 PTK7_CHICK | Q91048 gallus gall |
| 5 | 56.5 | 32.7 | 580 | 1 GGT1_ECOLI | P18956 escherichia |
| 6 | 53 | 30.6 | 360 | 1 VTPX_TTVI | P19374 thermoprote |
| 7 | 53 | 30.6 | 474 | 1 VTP3_TTVI | P19275 thermoprote |
| 8 | 52.5 | 30.3 | 243 | 1 YX42_MYCTU | O53392 mycobacteri |
| 9 | 52 | 30.1 | 514 | 1 CSA1_DICDI | P08796 dictyostell |
| 10 | 52 | 30.1 | 773 | 1 YHGF_ECOLI | P46837 escherichia |
| 11 | 52 | 30.1 | 952 | 1 YVRA_THETH | O56242 thermus the |
| 12 | 50 | 28.9 | 438 | 1 YDR6_SCHPO | O13741 schizosacch |
| 13 | 50 | 28.9 | 481 | 1 PYR5_MOUSE | P13439 mus musculu |
| 14 | 50 | 28.9 | 848 | 1 YAM6_SCHPO | Q10061 schizosacch |
| 15 | 49 | 28.3 | 925 | 1 W70T_HUMAN | P57737 homo sapien |
| 16 | 49 | 28.3 | 281 | 1 HIS2_ARATH | O82768 arabidopsis |
| 17 | 49 | 28.3 | 299 | 1 YJH9_YEAST | P47032 saccharomyc |
| 18 | 49 | 28.3 | 384 | 1 UDG_STEPRN | O57346 streptococc |
| 19 | 49 | 28.3 | 466 | 1 EXU1_DROVI | O24747 drosophilila |
| 20 | 49 | 28.3 | 1070 | 1 PTK7_HUMAN | Q13088 homo sapien |
| 21 | 48.5 | 28.0 | 2363 | 1 SPCO_MOUSE | O62651 mus musculu |
| 22 | 48 | 27.7 | 172 | 1 YH74_METHH | O27862 methanobact |
| 23 | 48 | 27.7 | 299 | 1 MRAN_MYCPU | O98875 mycoplasma |
| 24 | 48 | 27.7 | 326 | 1 MTC2_CHYPI | P31118 parametium |
| 25 | 48 | 27.7 | 349 | 1 RECA_AZOVI | P29294 azotobacter |
| 26 | 48 | 27.7 | 1744 | 1 CO4_HUMAN | P01028 homo sapien |
| 27 | 48 | 27.7 | 1888 | 1 CALE_CHICK | P32018 gallus gall |
| 28 | 48 | 27.7 | 2491 | 1 MPRI_HUMAN | P11717 homo sapien |
| 29 | 47.5 | 27.5 | 1130 | 1 ITAC_HUMAN | P33329 homo sapien |
| 30 | 47 | 27.2 | 189 | 1 TBP_PYROCC | P58127 pyrodictium |
| 31 | 47 | 27.2 | 390 | 1 LPXB_HAEIN | P45011 haemophilus |
| 32 | 47 | 27.2 | 480 | 1 PYR5_HUMAN | P11172 homo sapien |
| 33 | 47 | 27.2 | 1102 | 1 TRI3_YEAST | Q03660 saccharomyc |

ALIGNMENTS

| Result ID | Score | Query Match | Length | ID | Description |
|-----------|-------|-------------|--------|--------------|---------------------|
| 1 | 155 | 89.6 | 170 | 1 FMC1_ECOLI | P02871 escherichia |
| 2 | 153 | 88.4 | 171 | 1 FMS1_ECOLI | P25730 escherichia |
| 3 | 60.5 | 35.0 | 714 | 1 YFE1_YEAST | P43556 saccharomyc |
| 4 | 58 | 33.5 | 1051 | 1 PTK7_CHICK | Q91048 gallus gall |
| 5 | 56.5 | 32.7 | 580 | 1 GGT1_ECOLI | P18956 escherichia |
| 6 | 53 | 30.6 | 360 | 1 VTPX_TTVI | P19374 thermoprote |
| 7 | 53 | 30.6 | 474 | 1 VTP3_TTVI | P19275 thermoprote |
| 8 | 52.5 | 30.3 | 243 | 1 YX42_MYCTU | O53392 mycobacteri |
| 9 | 52 | 30.1 | 514 | 1 CSA1_DICDI | P08796 dictyostell |
| 10 | 52 | 30.1 | 773 | 1 YHGF_ECOLI | P46837 escherichia |
| 11 | 52 | 30.1 | 952 | 1 YVRA_THETH | O56242 thermus the |
| 12 | 50 | 28.9 | 438 | 1 YDR6_SCHPO | O13741 schizosacch |
| 13 | 50 | 28.9 | 481 | 1 PYR5_MOUSE | P13439 mus musculu |
| 14 | 50 | 28.9 | 848 | 1 YAM6_SCHPO | Q10061 schizosacch |
| 15 | 49 | 28.3 | 925 | 1 W70T_HUMAN | P57737 homo sapien |
| 16 | 49 | 28.3 | 281 | 1 HIS2_ARATH | O82768 arabidopsis |
| 17 | 49 | 28.3 | 299 | 1 YJH9_YEAST | P47032 saccharomyc |
| 18 | 49 | 28.3 | 384 | 1 UDG_STEPRN | O57346 streptococc |
| 19 | 49 | 28.3 | 466 | 1 EXU1_DROVI | O24747 drosophilila |
| 20 | 49 | 28.3 | 1070 | 1 PTK7_HUMAN | Q13088 homo sapien |
| 21 | 48.5 | 28.0 | 2363 | 1 SPCO_MOUSE | O62651 mus musculu |
| 22 | 48 | 27.7 | 172 | 1 YH74_METHH | O27862 methanobact |
| 23 | 48 | 27.7 | 299 | 1 MRAN_MYCPU | O98875 mycoplasma |
| 24 | 48 | 27.7 | 326 | 1 MTC2_CHYPI | P31118 parametium |
| 25 | 48 | 27.7 | 349 | 1 RECA_AZOVI | P29294 azotobacter |
| 26 | 48 | 27.7 | 1744 | 1 CO4_HUMAN | P01028 homo sapien |
| 27 | 48 | 27.7 | 1888 | 1 CALE_CHICK | P32018 gallus gall |
| 28 | 48 | 27.7 | 2491 | 1 MPRI_HUMAN | P11717 homo sapien |
| 29 | 47.5 | 27.5 | 1130 | 1 ITAC_HUMAN | P33329 homo sapien |
| 30 | 47 | 27.2 | 189 | 1 TBP_PYROCC | P58127 pyrodictium |
| 31 | 47 | 27.2 | 390 | 1 LPXB_HAEIN | P45011 haemophilus |
| 32 | 47 | 27.2 | 480 | 1 PYR5_HUMAN | P11172 homo sapien |
| 33 | 47 | 27.2 | 1102 | 1 TRI3_YEAST | Q03660 saccharomyc |

```
CC -!- INDUCTION: CFA/I FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF
CC THE POSITIVE REGULATOR CFAD.
CC -!- SIMILARITY: TO THE CS1 FIMBRIAL SUBUNIT A (CSOA).
CC -----
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CC -----
DR EMBL; M55661; AAC41415.1; -.
DR PIR; A05889; YQECCL.
KW Fimbria; Antigen; Plasmid; Signal.
FT SIGNAL 1 23
FT CHAIN 24 170 CFA/I FIMBRIAL SUBUNIT B.
FT CONFLICT 37 37 V -> A (IN REF. 2).
FT CONFLICT 76 76 D -> N (IN REF. 3).
FT CONFLICT 97 97 S -> A (IN REF. 3).
SQ SEQUENCE 170 AA; 17461 MW; 924347F07F33CDAB CRC64;

Query Match 89.6%; Score 155; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qv 1 VEKNITVTASVDPTIDLLQAGSALPSAVALTYSPA 36
| | | | | | | | | | | | | | | | | | | | | |
Db 24 VEKNITVTASVDPTIDLLQAGSALPSAVALTYSPA 59

RESULT 2
FMS1_ECOLI STANDARD; PRT; 171 AA.
AC P25730.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CS1 fimbrial subunit A precursor (CS1 pilin).
CN CSOA OR COOA.
OS Escherichia coli.
OG Plasmid pDEP23, and Plasmid pEU605.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O139:H28; PLASMID=pDEP23;
RX MEDLINE=91157443; PubMed=1679404;
RA Jordi B.J.A.M., van Vliet A.H.M., Willshaw G.A.,
RA van der Zeijst B.A.M., Gaastera W.;
RT "Analysis of the first two genes of the CS1 fimbrial operon in human
RT enterotoxigenic Escherichia coli of serotype O139:H28";
RL FEMS Microbiol. Lett. 64:265-270(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H16; PLASMID=pEU605;
RX MEDLINE=91034170; PubMed=1977705;
RA Perez-Casal J., Swartley J.S., Scott J.R.;
RA "Gene encoding the major subunit of CS1 pili of human enterotoxigenic
RT Escherichia coli.";
RL Infect. Immun. 58:3594-3600(1990).
RN [3]
RP SEQUENCE OF 24-42.
RC STRAIN=60R75;
RX MEDLINE=90036735; PubMed=2572583;
RA Hall R.H., Maneval D.R. Jr., Collins J.H., Theibert J.L.,
RA Levine M.M.;
RT "Purification and analysis of colonization factor antigen 1, coli
RT surface antigen 1, and coli surface antigen 3 fimbriae from
RT enterotoxigenic Escherichia coli.";
RL J. Bacteriol. 171:6372-6374(1989).
CC -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING

FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
-!- INDUCTION: CS1 FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF THE
POSITIVE REGULATOR RNS.
-!- SIMILARITY: TO THE CFA/I FIMBRIAL SUBUNIT B (CFAB).
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-----
DR EMBL; X62879; CAA44673.1; -.
DR EMBL; M58550; AAA23596.1; -.
DR PIR; A41467; A41467.
DR PIR; S19003; S19003.
KW Fimbria; Signal; Plasmid.
FT SIGNAL 1 23
FT CHAIN 24 171 CS1 FIMBRIAL SUBUNIT A.
FT CONFLICT 28 28 I -> E (IN REF. 3).
SQ SEQUENCE 171 AA; 17542 MW; 46E70BE7053DBE13 CRC64;

Query Match 88.4%; Score 153; DB 1; Length 171;
Best Local Similarity 83.3%; Pred. No. 4.2e-14;
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qv 1 VEKNITVTASVDPTIDLLQAGSALPSAVALTYSPA 36
| | | | | | | | | | | | | | | | | | | | | |
Db 24 VEKNITVTASVDPTIDLLQAGSALPSAVALTYSPA 59

RESULT 3
YFE7_YEAST STANDARD; PRT; 714 AA.
AC P43556;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 82.2 kDa protein in EMP47-SEC53 intergenic region.
CN YFL047W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
CC -!- SIMILARITY: CONTAINS 1 DEP DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PCH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
CC -----
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-----
DR EMBL; D50617; BAA09194.1; -.
DR SGD; S0001847; YFL047W.
DR InterPro; IPR001060; Cdc15_Fes_C1P4.
DR InterPro; IPR000591; DEP.
```


RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 [3]
 RP SEQUENCE OF 1-362 FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=94316500; PubMed=8041620;
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
 RT "Analysis of the *Escherichia coli* genome. V. DNA sequence of the
 RT region from 76.0 to 81.5 minutes.";
 RL Nucleic Acids Res. 22:2576-2586(1994).
 [4]
 RP MUTAGENESIS.
 RX MEDLINE=91800553; PubMed=1360205;
 RA Hashimoto M., Suzuki H., Nohara S., Kumagai H.;
 RT "Escherichia coli gamma-glutamyltransferase mutants deficient in
 RT processing to subunits.";
 RL Biochem. Biophys. Res. Commun. 189:173-178(1992).
 CC -1- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid =
 CC peptide + 5-L-glutamyl-amino acid.
 CC -1- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A
 CC PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
 CC -1- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE
 CC SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.
 CC -1- SUBCELLULAR LOCATION: Peroxisomic.
 CC -1- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
 CC
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 CC
 DR EMBL; M28722; AAA23869.1; -;
 DR EMBL; U18997; AAA58245.1; -;
 DR EMBL; AE000421; AAC76472.1; -;
 DR EMBL; U00039; AAB18422.1; -;
 DR PIR; JVO028; EKECEX.
 DR MEROPS; T03.001; -;
 DR EcoGene; EG10374; ggt.
 DR InterPro; IPR000101; Gglutnrsptdase.
 DR Pfam; PF01019; G_glu_transpept; 1.
 DR PRINTS; PR01210; GGTTRANSPTASE.
 DR TIGRPFAMs; TIGR00066; g_glu_trans; 1.
 DR PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.
 DR Transference; Acyltransferase; Periplasmic; Zymogen; Signal;
 KW Glutathione biosynthesis; Complete proteome.
 FT SIGNAL 1 25
 FT CHAIN 26 390 GAMMA-GLUTAMYLTRANSFERASE LARGE CHAIN.
 FT CHAIN 391 580 GAMMA-GLUTAMYLTRANSFERASE SMALL CHAIN.
 FT BINDING 465 465 GAMMA-GLUTAMYL (POTENTIAL).
 FT MUTAGEN 513 513 R->A: NOT PROCESSED INTO ITS SUBUNITS.
 FT MUTAGEN 571 571 R->G: NOT PROCESSED INTO ITS SUBUNITS.
 SQ SEQUENCE 580 AA; 61768 MW; 772F652EBA2A5F00 CRC64;
 Query Match 32.7%; Score 56.5; DB 1; Length 580;
 Best Local Similarity 40.0%; Pred. No. 4;
 Matches 14; Conservative 9; Mismatches 7; Indels 5; Gaps 1;
 QY 7 VTASVDPD-----IDLQDGSALPSAVALTYSPA 36
 DB 50 MVASVDAATQGVQVILKEGNAVDAAVAVGYALA 84
 RESULT 6
 VTPX_TTV1
 ID VTPX TTV1 STANDARD; PRT; 360 AA.
 AC P19274;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Viral protein TPX.
 OS Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
 OC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
 OC Lipothirixvirus.
 OX NCBI_TaxID=10480;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174928; PubMed=2308830;
 RA Neumann H., Zillig W.;
 RT "The TTV1-encoded viral protein TPX: primary structure of the gene
 RT and the protein.";
 RL Nucleic Acids Res. 18:195-195(1990).
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 CC
 DR EMBL; X14855; CAA33002.1; -;
 DR PIR; S12850; S12850.
 KW Repeat.
 FT DOMAIN 278 353 3 THR-PRO REPEATS REGIONS AND TWO NEAR
 FT IDENTICAL REPEATS.
 FT REPEAT 270 291 THR-PRO(N).
 FT REPEAT 292 301 THR-PRO(N).
 FT REPEAT 302 322 THR-PRO(N).
 FT REPEAT 323 332 THR-PRO(N).
 FT REPEAT 333 353 THR-PRO(N).
 SQ SEQUENCE 360 AA; 38214 MW; EF54FBCB753ED1CA CRC64;
 Query Match 30.6%; Score 53; DB 1; Length 360;
 Best Local Similarity 42.1%; Pred. No. 6.9;
 Matches 16; Conservative 7; Mismatches 9; Indels 6; Gaps 2;
 QY 3 KNITVTAS-----VDPTIDLLQDGSALPSAVALTYSP 35
 DB 63 QSITITASSGTFNIDFTIALYNGSSY-SNLTLCVSP 99
 RESULT 7
 VTP3_TTV1V
 ID VTP3 TTV1V STANDARD; PRT; 474 AA.
 AC P19275;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Viral protein TPX.
 OS Thermoproteus tenax virus 1 (strain VT3) (TTV1).
 OC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
 OC Lipothirixvirus.
 OX NCBI_TaxID=10481;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245666; PubMed=2336394;
 RA Neumann H., Zillig W.;
 RT "Nucleotide sequence of the viral protein TPX of the TTV1 variant
 RT VT3.";
 RL Nucleic Acids Res. 18:2171-2171(1990).
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 CC
 DR EMBL; X14717; CAA32838.1; -;

DR PIR; S06686; S06686.
 KW Repeat.
 FT DOMAIN 278 467 3 THR-PRO REPEATS REGIONS AND TWO NEAR
 IDENTICAL REPEATS.
 FT REPEAT 278 367 THR-PRO (N).
 FT REPEAT 368 377 THR-PRO (N).
 FT REPEAT 378 436 THR-PRO (N).
 FT REPEAT 437 446 THR-PRO (N).
 FT REPEAT 447 467 THR-PRO (N).
 SQ SEQUENCE 474 AA; 49507 MW; 1037109136598829 CRC64;

Query Match 30.6%; Score 53; DB 1; Length 474;
 Best Local Similarity 42.1%; Pred. No. 9.6;
 Matches 16; Conservative 7; Mismatches 9; Indels 6; Gaps 2;

3 KNTVTAS-----VDPITDLDAGSALPSAVALTSP 35
 63 QSTITVASGTPNIDPTIALYNNSSY-SNLTLVGSP 99

RESULT 8
 YX42_MYCTU STANDARD; PRT; 243 AA.
 AC 053392;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative methyltransferase RV3342 (EC 2.1.1.1.-).
 GN RV3342 OR MT3445 OR MTV016.42.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Sulterson J.E., Taylor K., Whitehead S., Barrell B.G.;
 "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 Nature 393:537-544(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bisht W.;
 "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
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DR EMBL; AL021841; CA117114.1; ALT_INIT.
 DR EMBL; AE007151; AAK47789.1; -.
 DR TIGR; MT3445; -.

DR Tuberculin; RV3342; -.
 DR InterPro; IPR000051; SAM_bind.
 KW Hypothetical protein; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 243 AA; 26640 MW; BD755CG5AF70C4D3 CRC64;

Query Match 30.3%; Score 52.5; DB 1; Length 243;
 Best Local Similarity 45.2%; Pred. No. 5.1;
 Matches 14; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

1 VKNTVTASVPTDLDAGSALPSAVALT 31
 57 VERGLDVA-VDPIDMDVLRALPQTVAL 86

RESULT 9
 CSA_DICDI STANDARD; PRT; 514 AA.
 AC P08796; P19408;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Contact site A protein precursor (CSA) (Membrane-associated
 DE glycoprotein gp80) (Cell adhesion molecule gp80).
 GN CSA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellidae; Dictyostelium.
 NCBI_TaxID=44689;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Noegel A., Gerisch G., Stadler J., Westphal M.;
 RT "Complete sequence and transcript regulation of a cell adhesion
 RT protein from aggregating Dictyostelium cells.";
 RL EMBL J. 5:1473-1476(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=89105362; PubMed=3063296;
 RA Siu C.H., Wong L.M., Lam T.Y., Kamboj R.K., Choi A., Cho A.;
 RT "Molecular mechanisms of cell-cell interaction in Dictyostelium
 RT discoideum.";
 RN Biochem. Cell Biol. 66:1089-1099(1988).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=AX2;
 RC MEDLINE=92406924; PubMed=1326559;
 RA Desbates L., Lam T.Y., Wong L.M., Siu C.H.;
 RT "Identification of a unique cAMP-response element in the gene
 RT encoding the cell adhesion molecule gp80 in Dictyostelium
 RT discoideum.";
 RL J. Biol. Chem. 267:19655-19664(1992).
 RN [4]
 RN SEQUENCE OF 20-49.
 RA Wong L.M., Siu C.H.;
 RT "Cloning of cDNA for the contact site A glycoprotein of Dictyostelium
 RT discoideum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4248-4252(1986).
 RN [5]
 RN CELL-BINDING DOMAIN.
 RP MEDLINE=89034443; PubMed=3182938;
 RX Kamboj R.K., Wong L.M., Lam T.Y., Siu C.H.;
 RA "Mapping of a cell-binding domain in the cell adhesion molecule gp80
 RT of Dictyostelium discoideum.";
 RL J. Cell Biol. 107:1835-1843(1988).
 RN [6]
 RN GPI-ANCHOR.
 RP MEDLINE=89251561; PubMed=2721485;
 RX Stadler J., Keenan T.W., Bauer G., Gerisch G.;
 RA "The contact site A glycoprotein of Dictyostelium carries
 RT a phospholipid anchor of a novel type.";
 RL EMBL J. 8:371-377(1989).
 CC -1- FUNCTION: THIS CELL-SURFACE GLYCOPROTEIN MEDIATES CELL-CELL
 CC BINDING VIA HOMOPHILIC INTERACTION.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR

CC THAT CONTAINS A PHOSPHOCERAMIDE MOIETY. SUCH ANCHOR MEDIATES A
CC FAST AND LONG PERSISTENCE CELL ADHESION OF THE PROTEIN.
CC -1 DEVELOPMENTAL STAGE: RESTRICTED TO THE AGGREGATION STAGE OF
CC DEVELOPMENT OF D. DISCOIDEUM.
CC -1- PTM: ACYLATED, PHOSPHORYLATED ON SERINE AND N-GLYCOSYLATED WITH
CC -1- MISCELLANEOUS: THE EXPRESSION OF THIS STRINGENTLY REGULATED
CC PROTEIN DURING CELL DEVELOPMENT IS MEDIATED THROUGH CELL-SURFACE
CC CAMP RECEPTORS.
CC -1- SIMILARITY: THE C-TERMINAL REGION CONTAINS CLUSTERS OF PROLINE
CC REGULARLY ALTERNATING WITH A HYDROXYAMINO ACID AND SHOWS
CC SIMILARITY TO THE HINGE REGION OF IMMUGLOBULINS. THIS DOMAIN
CC MIGHT ACT AS A SPACER TO ELEVATE SITES ACTIVE IN CELL CONTACT
CC INTO THE EXTRACELLULAR SPACE.
CC
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CC
CC EMBL; X04004; CAA27634.1; -
CC EMBL; M36545; AAA33212.1; -
CC EMBL; X66483; CAA47110.1; -
CC PIR; A23951; A23951.
CC PIR; A26410; A26410.
CC PIR; A31643; A31643.
CC PIR; A22066; S22066.
CC PIR; A44100; A44100.
CC Dictyob; D002005; csaA.
CC InterPro; IPR002909; IPT_TIG.
CC Pfam; PF01843; TIG; 3.
CC Cell adhesion; Glycoprotein; Membrane; Phosphorylation; Repeat;
CC GPI-anchor; Lipoprotein; Signal.
CC
CC SIGNAL 1 19
CC CHAIN 20 492 CONTACT SITE A PROTEIN.
CC PROPEP 493 514 REMOVED IN MATURE FORM (POTENTIAL).
CC DOMAIN 20 453 GLOBULAR (POTENTIAL).
CC DOMAIN 454 485 PRO-RICH (HINGE STRUCTURE).
CC DOMAIN 462 479 2 X 8 AA REPEATS, PRO-RICH.
CC REPEAT 462 469 1.
CC REPEAT 472 479 2.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC LIPID 492 492 GPI-ANCHOR (POTENTIAL).
CC CONFLICT 216 216 V -> G (IN REF. 1).
CC SEQUENCE 514 AA; 53696 MW; 96A1C7CF42FEC096 CRC64;

Query Match 30.1%; Score 52; DB 1; Length 514;
Best Local Similarity 26.5%; Pred. No. 15;
Matches 9; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2 EKNITVTASVDPTIDLLQADGSAIPSAVALTYSP 35
DB 251 ESNITITAKASTGVDMIVLDNQGNOQPTFTYTPN 284

RESULT 10
YHGF_ECOLI
ID YHGF_ECOLI STANDARD; PRT; 773 AA.
AC P46837; P76689;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein YhgF.
GN YHGF OR H407.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R.; Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10491123;
RA Fountoulakis M., Takacs M.F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography";
RL Electrophoresis 20:2181-2195(1999).
CC -1- SIMILARITY: STRONG, TO H.INFLUENZA H10568.
CC -1- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
CC
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CC
CC EMBL; U18997; AAA58204.1; ALT_FRAME.
CC EMBL; U18997; AAA58205.1; ALT_FRAME.
CC EMBL; AE000416; AAC76432.1; ALT_INIT.
CC HSSP; P05055; ISRO.
CC EcoGene; EGI2932; yhgF.
CC InterPro; IPR003029; SI.
CC Pfam; PF00575; SI; 1.
CC SMART; SM00316; SI; 1.
CC PROSITE; PS0126; SI; 1.
CC RNA-binding; Complete proteome.
CC DOMAIN 651 720 SI MOTIF.
CC CONFLICT 754 755 QP -> HA (IN REF. 1; AAA58205).
CC SEQUENCE 773 AA; 85119 MW; EA49ED952A8229 CRC64;

Query Match 30.1%; Score 52; DB 1; Length 773;
Best Local Similarity 37.9%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 5 ITVTASVDPTIDLLQADGSAIPSAVALTY 33
DB 117 IATEAGLEPLADLLWSDPSHTPEVAAQY 145

RESULT 11
UVRA_THETH
ID UVRA_THETH STANDARD; PRT; 952 AA.
AC Q56242;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Excinuclease ABC subunit A.
GN UVRA.
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=96257202; PubMed=8675016;
RA Yamamoto N., Kato R., Kuramitsu S.;
RT "Cloning, sequencing and expression of the uvrA gene from an
RT extremely thermophilic bacterium, Thermus thermophilus HB8.";

RL Gene 171:103-106(1996).
 CC - FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE
 CC AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-
 CC STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
 CC - SUBUNIT: CONSISTS OF THREE SUBUNITS, UVRA, UVRB AND UVRC.
 CC - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC - SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
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 DR EMBL: D49911; BAA08652.1; -
 DR InterPro: IPR003439; ABC_transport.
 DR Pfam: PF00005; ABC_tran; 2.
 DR Prodom: PD000006; ABC_transport; 1.
 DR TIGRfam: TIGR00630; Uvra; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
 KW SOS response; Excision nuclease; DNA repair; ATP-binding; Repeat;
 KM DNA-binding; Zinc-finger.
 FT NP_BIND 31 38 ATP (POTENTIAL).
 FT NP_BIND 643 650 ATP (POTENTIAL).
 FT ZN_FING 253 280 C4-TYPE.
 FT ZN_FING 742 768 C4-TYPE.
 SQ SEQUENCE 952 AA; 105232 MW; FBE2338B45CA96DD CRC64;
 Query Match 30.1%; Score 52; DB 1; Length 952;
 Best Local Similarity 35.6%; Pred. No. 30;
 Matches 16; Conservative 6; Mismatches 11; Indels 12; Gaps 2;
 QY 1 VENKITASVDPITD-----LOADGSAIPSAVALTYSP 35
 DB 890 IEHLVDVKTADWVITLGPFGDGRGEIVAGT--PREVALTSP 932
 ID YDR6 SCHPO STANDARD; PRT; 438 AA.
 C 013741;
 15-JUN-2002 (Rel. 41, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Hypothetical RNA-binding protein Cl6E8.06c in chromosome I.
 GN SPAC16E8.06c.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI_TaxID=4896;
 GN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21846401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor A., Cronin A., Davis P., Fellwell T., Frazer A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Butler S., Saunders D., Seeger K., Sharp S.,
 RA Stelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,

RA Weljens I., Vanstelele E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambolt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nure P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC - SIMILARITY: TO YEAST NOP12.
 CC - SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
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 DR EMBL: Z98529; CAB11047.1; -
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 2.
 DR SMART: SMO0360; RRM; 2.
 DR PROSITE: PS00102; RRM; 2.
 DR PROSITE: PS00303; RRM_RNP_1; 1.
 KW Hypothetical protein; RNA-binding; Repeat.
 FT DOMAIN 164 262 RNA-BINDING (RRM) 1.
 FT DOMAIN 270 348 RNA-BINDING (RRM) 2.
 FT DOMAIN 20 23 POLY-SER.
 FT DOMAIN 81 90 POLY-LYS.
 SQ SEQUENCE 438 AA; 49381 MW; 3E943401P95E7C12 CRC64;
 Query Match 28.9%; Score 50; DB 1; Length 438;
 Best Local Similarity 34.6%; Pred. No. 23;
 Matches 9; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 5 ITVTASVDPITDLOADGSAIPSAVA 30
 DB 19 LSSSNVDPITLTLFOSKPIPKPVA 44
 ID PYR5 MOUSE STANDARD; PRT; 481 AA.
 C 013439; G99L26;
 01-JAN-1990 (Rel. 13, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate
 DE phosphoribosyltransferase (EC 2.4.2.10) (OPRase); Orotidine 5'-
 DE phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)].
 GN Umps.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 GN [1]
 RP SEQUENCE FROM N.A.
 RA Strusberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 216-481 FROM N.A.
 RX MEDLINE=86140253; PubMed=2419341;
 RA Chmielec C.A., Langdon S.D., Chae C.B., Jones M.E.;
 RT "Expression and sequence analysis of a cDNA encoding the orotidine-5'-
 RT monophosphate decarboxylase domain from Ehrlich ascites uridylylate
 RT synthase";
 RT J. Biol. Chem. 261:4276-4282(1986).

```
CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate = orotate
CC + 5 phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Pyrimidine biosynthesis; fifth and sixth (last) steps.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
CC OMP DECARBOXYLASE FAMILY.
CC -----
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CC -----
DR EMBL: BC003887; AA03887.1;
DR EMBL: M29195; AAA39859.1;
DR PR: A25323; DCM50P.
DR HSP: P03962; IDQP.
DR MGD: MGI:1298388; Umps.
DR InterPro: IPR001754; OMPdecase.
DR InterPro: IPR002375; Pp/PY rp trans.
DR InterPro: IPR008836; PRTtransferase.
DR InterPro: IPR004467; Pyre.
DR Pfam: PF00215; OMPdecase; 1.
DR TIGRfams: TIGR00336; pyre; 1.
DR PROSITE: PS00156; OMPDECASE; 1.
DR PROSITE: PS00103; PUR PYR PR TRANSFER; 1.
KW Pyrimidine biosynthesis; Multifunctional enzyme; Transferase;
KW Glyoxylate transferase; Lyase; decarboxylase.
FT DOMAIN 1 214 OPRASE.
FT DOMAIN 215 220 DOMAIN LINKER.
FT DOMAIN 221 481 OMPDECASE.
FT ACT_SITE 314 314 BY SIMILARITY.
SQ SEQUENCE 481 AA; 52292 MW; 761C7EF7960C9C59 CRC64;

Query Match 28.9%; Score 50; DB 1; Length 481;
Best Local Similarity 35.5%; Pred. No. 25;
Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VEKNITVTASVPTIDLLQADGSAALPSAVAL 31
Db 122 IEDVVVTCGASVLETVLQKGLKVTDAIVL 152

RESULT 14
YAM6 SCHPO STANDARD; PRT; 848 AA.
AC Q10061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock protein 70 homolog precursor.
GN SPAC1F5.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4996;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 972;
EX MESLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holtova S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymopiez B.,
RA Weljens J., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Mottier S.,
RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fotsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002). Endoplasmic reticulum lumen (Potential).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL: Z68136; CAA92234.1;
DR InterPro: IPR000886; HSP target.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR ProDom: PD000089; HSP70; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00297; HSP70_1; FALSE_NEG.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR Hypothetical protein; Endoplasmic reticulum; Signal; ATP-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 848 HEAT SHOCK PROTEIN 70 HOMOLOG.
FT SITE 845 848 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 848 AA; 94897 MW; A1963FD4253F38F3 CRC64;

Query Match 28.9%; Score 50; DB 1; Length 848;
Best Local Similarity 27.3%; Pred. No. 50;
Matches 9; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VEKNITVTASVPTIDLLQADGSAALPSAVALTY 33
Db 202 IEYSLRSFSTDPTNYIIVDSGSGSTSATVISP 234

RESULT 15
W70T_HUMAN STANDARD; PRT; 925 AA.
ID W70T_HUMAN
AC P57737;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 70 kDa WD-repeat tumor rejection antigen homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Oka T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoqai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
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DE precursor;
GN YJL079C OR J1022.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI TaxID 4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5788C;
RA MEDLINE=96093911; PubMed=7483841;
RA Miosga T., Schaaff-Gerstenschlaeger I., Chaltwatzis N., Baur A.,
RA Holes E., Fournier C., Schmitt S., Velten C., Wilhelm N.,
RA Zimmermann F.K.;
RT "Sequence analysis of a 33.1 kb fragment from the left arm of
RT Saccharomyces cerevisiae chromosome X, including putative proteins
RT with leucine zippers, a fungal Zn(II)-Cys6 binuclear cluster domain
RT and a putative alpha 2-SCB-alpha 2 binding site.";
RL Yeast 11:681-689(1995).
CC 1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL; Z49154; CAA89372.1; -
DR EMBL; X83502; CAA58491.1; -
DR EMBL; X88851; CAA61315.1; -
DR HSSP; PC4284; 1CFE.
DR SGD; S0003615; YJL079C.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP_1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRI_SC1; 1.
DR PROSITE; PS01010; SCP_AG5_PRI_SC2; 1.
KW Hypothetical protein; Signal; POTENTIAL.
FT SIGNAL 1 19
FT CHAIN 20 299 HYPOTHETICAL PROTEIN YJL079C.
FT DOMAIN 102 165 ALA/SER/THR-RICH.
SQ SEQUENCE 299 AA; 30634 MW; A316769CA87C5679 CRC64;

Query Match 28.3%; Score 49; DB 1; Length 299;
Best Local Similarity 31.4%; Pred. No. 20;
Matches 11; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 2 EKNTVTASVPTDLDQAGSALPSAVALTYSFA 36
Db 104 DSTTTLTSSSTSSQSLAQTTSITPAAASTTSTPA 138

RESULT 18
UDG_STREN
ID UDG_STREN STANDARD; PRT; 394 AA.
AC Q57346; Q54610; P72519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UDP-glucose 6 dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase)
DE (UDP-GlcDH) (UDPGDH).
GN CAP3A OR CPS3D.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI TaxID:1113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-406 / Type 3;
```

```
RX MEDLINE=95014083; PubMed=7929009;
RA Arrecubieta C., Lopez R., Garcia E.;
RT "Molecular characterization of cap3A, a gene from the operon required
RT for the synthesis of the capsule of Streptococcus pneumoniae type 3;
RT sequencing of mutations responsible for the unencapsulated phenotype
RT and localization of the capsular cluster on the pneumococcal
RT chromosome.";
RL J. Bacteriol. 176:6375-6383(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-406 / Type 3;
RA MEDLINE=96144241; PubMed=8566758;
RA Arrecubieta C., Garcia E., Lopez R.;
RT "Sequence and transcriptional analysis of a DNA region involved in
RT the production of capsular polysaccharide in Streptococcus pneumoniae
RT type 3.";
RL Gene 167:1-7(1995).
RN [3]
RP REVISIONS TO 129 AND 228.
RA Garcia E., Arrecubieta C., Munoz R., Mollerach M., Lopez R.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=WU2 / Serotype 3;
RA MEDLINE=95173611; PubMed=7869055;
RA Dillard J.P., Vandersea M.W., Yother J.;
RT "Characterization of the cassette containing genes for type 3
RT capsular polysaccharide biosynthesis in Streptococcus pneumoniae.";
RL J. Exp. Med. 181:973-983(1995).
CC 1- FUNCTION: CATALYZES THE FORMATION OF UDP-GLUCURONIC ACID WHICH IS
CC REQUIRED FOR CAPSULAR HYALURONIC ACID SYNTHESIS. DIRECTLY
CC RESPONSIBLE FOR THE TRANSFORMATION OF SOME UNENCAPSULATED
CC SEROTYPE-3 SP MUTANTS TO THE ENCAPSULATED PHENOTYPE.
CC 2- CATALYTIC ACTIVITY: UDP-glucose + 2 NAD(+) + H(2)O -> UDP
CC glucuronate + 2 NADH.
CC 3- PATHWAY: HYALURONATE SYNTHESIS.
CC 4- SIMILARITY: BELONGS TO THE UDP-GLUCOSE/GDP-MANNOSE DEHYDROGENASES
CC FAMILY.
CC -----
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CC -----
DR EMBL; Z47210; CAA87403.1; -
DR EMBL; Z12159; CAA78147.1; -
DR EMBL; U15171; AAC43311.1; -
DR InterPro; IPR001732; UDGP_MGDP dh.
DR Pfam; PF00984; UDGP_MGDP dh; 1.
DR Pfam; PF03720; UDGP_MGDP dh C; 1.
DR Pfam; PF03721; UDGP_MGDP dh_N; 1.
KW Oxidoreductase; NAD.
FT NP BIND 2 19
FT ACT SITE 259 259 BY SIMILARITY.
FT CONFLICT 215 215 R -> A (IN REF. 4).
FT CONFLICT 247 247 Y -> D (IN REF. 4).
SQ SEQUENCE 394 AA; 44697 MW; C68671ED88140FC3 CRC64;

Query Match 28.3%; Score 49; DB 1; Length 394;
Best Local Similarity 27.7%; Pred. No. 28;
Matches 13; Conservative 8; Mismatches 8; Indels 18; Gaps 1;

QY 1 VEKNITVTASVDPT-----IDLQAGSALPSAV 29
Db 55 VEKELNLEASLDPAHYKQVEYAIATPTNYDVLNQFDTSVEAAI 101

RESULT 19
EXU_DROVI
ID EXU_DROVI STANDARD; PRT; 486 AA.
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FT DOMAIN 606 671 IG-LIKE C2-TYPE DOMAIN 7.
 FT DOMAIN 796 1066 PROTEIN KINASE; INACTIVE.
 FT DISULFID 53 101 BY SIMILARITY.
 FT DISULFID 150 200 BY SIMILARITY.
 FT DISULFID 246 301 BY SIMILARITY.
 FT DISULFID 343 391 BY SIMILARITY.
 FT DISULFID 433 481 BY SIMILARITY.
 FT DISULFID 524 570 BY SIMILARITY.
 FT DISULFID 613 664 BY SIMILARITY.
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 92 92 P -> R (IN REF. 2 AND 3).
 FT CONFLICT 147 147 K -> T (IN REF. 2 AND 3).
 FT CONFLICT 207 207 S -> G (IN REF. 2 AND 3).
 FT CONFLICT 495 496 VL -> RV (IN REF. 2 AND 3).
 FT CONFLICT 515 515 G -> E (IN REF. 2 AND 3).
 FT CONFLICT 881 881 E -> G (IN REF. 2 AND 3).
 FT CONFLICT 969 969 A -> P (IN REF. 2 AND 3).
 FT CONFLICT 992 992 S -> F (IN REF. 2 AND 3).
 SQ SEQUENCE 1070 AA; 47CDF25B8E369A5 CRC64;

Query Match 28.3%; Score 49; DB 1; Length 1070;
 Best Local Similarity 43.8%; Pred. No. 90;
 Matches 14; Conservative 3; Mismatches 11; Indels 4; Gaps 1;

QY 2 EKNITVTASV ---DPTDLQAGSALPSAV 29
 DB 517 DEATVPASATGKREPTIKWEGAGSSUPEW 548
 RESULT 21
 SPCO MOUSE
 ID SPCO MOUSE STANDARD; PRT; 2363 AA.
 AC Q62261;
 DT 01 NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1)
 DE (Beta II spectrin) (Fodrin beta chain).
 DE SPTBN1 OR SPTB2 OR SPNB2 OR SPNB-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] TuxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=93240985; PubMed=8479293;
 RA Ma Y., Zimmer W.E., Riederer B.M., Goodman S.R.;
 RT "The complete amino acid sequence for brain beta spectrin (beta fodrin): relationship to globin sequences."
 RL Brain Res. Mol. Brain Res. 18:87-89(1993).
 [2]
 RP STRUCTURE BY NMR OF 2199-2304.
 RX MEDLINE=94268558; PubMed=8208297;
 RA Macias M.J., Musacchio A., Ponstingl H., Nilges M., Saraste M.,
 RA Oschkinat H.;
 RT "Structure of the pleckstrin homology domain from beta-spectrin."
 RL Nature 369:675-677(1994).
 [3]
 RP STRUCTURE BY NMR OF 2199-2304.
 RX MEDLINE=97342712; PubMed=9199409;
 RA Nilges M., Macias M.J., O'Donoghue S.I., Oschkinat H.;
 RT "Automated NMR interpretation with ambiguous distance restraints:
 the refined NMR solution structure of the pleckstrin homology domain

RT from beta-spectrin."
 RL J. Mol. Biol. 269:408-422(1997).
 [4]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304.
 RX MEDLINE=96030773; PubMed=7588597;
 RA Hyvoenen M., Macias M.J., Nilges M., Oschkinat H., Saraste M.,
 RA Wilmanns M.;
 RT "Structure of the binding site for inositol phosphates in a PH domain."
 RL EMBO J. 14:4676-4681(1995).
 CC -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
 CC INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 CC THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CC CYTOSKELETON AT THE MEMBRANE.
 CC -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 CC ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 CC TETRAMERS.
 CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 17 SPECTRIN REPEATS.
 CC -----
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 CC -----
 DR EMBL; M74773; AAC42040.1; -;
 DR PDB; 1BTN; 08-MAR-96.
 DR PDB; 1MPH; 16-JUN-97.
 DR MGD; MGI:98388; Spnb2.
 DR InterPro; IPR001589; Actbind actinin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR02017; Spectrin.
 DR InterPro; IPR001605; Spectrin_PH.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00435; spectrin; 18.
 DR PRINTS; PR00683; SPECTRINPH.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS00019; ACTININ 1; 1.
 DR PROSITE; PS00020; ACTININ 2; 1.
 DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
 KW 3D-structure.
 KW DOMAIN 1 275 ACTIN-BINDING (BY SIMILARITY).
 FT DOMAIN 54 158 CH 1.
 FT DOMAIN 173 275 CH 2.
 FT REPEAT 276 384 SPECTRIN 1.
 FT REPEAT 385 498 SPECTRIN 2.
 FT REPEAT 499 608 SPECTRIN 3.
 FT REPEAT 609 714 SPECTRIN 4.
 FT REPEAT 715 819 SPECTRIN 5.
 FT REPEAT 820 925 SPECTRIN 6.
 FT REPEAT 926 1032 SPECTRIN 7.
 FT REPEAT 1033 1139 SPECTRIN 8.
 FT REPEAT 1140 1245 SPECTRIN 9.
 FT REPEAT 1246 1350 SPECTRIN 10.
 FT REPEAT 1351 1462 SPECTRIN 11.
 FT REPEAT 1463 1562 SPECTRIN 12.
 FT REPEAT 1563 1668 SPECTRIN 13.
 FT REPEAT 1669 1775 SPECTRIN 14.
 FT REPEAT 1776 1881 SPECTRIN 15.
 FT REPEAT 1882 1987 SPECTRIN 16.
 FT REPEAT 1988 2132 SPECTRIN 17.
 FT DOMAIN 2196 2306 PH.

SQ SEQUENCE 2363 AA; 274420 MW; 64C9E4BD26B8C7B8 CRC64;
 Query Match 28.0%; Score 48.5; DB 1; Length 2363;
 Best Local Similarity 42.4%; Pred. No. 2.7e+02;
 Matches 14; Conservative 3; Mismatches 13; Indels 3; Gaps 1;

QY 1 VERNITVTASVD--PTIDLLQADGSAIPSAVA 30
 DB 783 VKKHQDAEITVYRPIDTLHEQASALPQAH 815

RESULT 22
 YH74_METH STANDARD; PRT; 172 AA.
 AC 027802;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 Hypothetical protein M01774.
 MTH1774.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzaden R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pochler B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics."
 RL J. Bacteriol. 179:7135-7151(1997).
 CC 1- SIMILARITY: BELONGS TO THE UPF0025 FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE000932; AAB86240.1; -;
 DR InterPro; IPR004843; M-peptidase.
 DR InterPro; IPR004844; S/T phosphatase.
 DR InterPro; IPR000979; UPF0025.
 DR Pfam; PF00149; Metallophos; 1.
 DR TIGRPFAMs; TIGR00040; UPF0025; 1.
 DR PROSITE; PS01269; UPF0025; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 172 AA; 19223 MW; F59AB11A52318EF2 CRC64;

Query Match 27.7%; Score 48; DB 1; Length 172;
 Best Local Similarity 33.3%; Pred. No. 14;
 Matches 10; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 6 TVTASVPTIDLLQADGSAIPSAVAITYSP 35
 DB 134 TVPRLTPSVWVLRIDSEKLDIAETIRIGAP 163

RESULT 23
 MRAW_MYCPU STANDARD; PRT; 239 AA.
 AC 098075;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE S-adenosyl-methyltransferase mraw (EC 2.1.1.-).
 MRAW OR MYPU 4930.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chamberaud I., Helling R., Ferris S., Barde V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski H., Viart A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis."
 RL Nucleic Acids Res. 29:2145-2153(2001).
 CC 1- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase
 CC activity (by similarity).
 CC 1- SIMILARITY: BELONGS TO THE MRAW FAMILY.
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 CC -----
 DR EMBL; AL445564; CAC13666.1; -;
 DR MyPulst; MYPU_4930; -;
 DR InterPro; IPR002903; Bac_MetTrfase.
 DR Pfam; PF01795; Methyltransf 5; 1.
 DR ProDom; PD004685; Bac_MetTrfase; 1.
 DR TIGRPFAMs; TIGR00006; UPF0117; 1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 299 AA; 34245 MW; 2E0D65FD3FF6DCP CRC64;

Query Match 27.7%; Score 48; DB 1; Length 299;
 Best Local Similarity 30.6%; Pred. No. 27;
 Matches 11; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 VERNITVTASVPTIDLLQADGSAIPSAVAITYSPA 36
 DB 163 VAKGIVNRPIDTLELVIRRSIPALVLRKNDA 198

RESULT 24
 MTC2_CHVP1 STANDARD; PRT; 326 AA.
 AC P31118; Q84569;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Modification methylase CviA11 (EC 2.1.1.72) (adenine-specific
 DE methyltransferase CviA11) (M_CviA11).
 GN CviA11M OR A251R.
 OS Paramesidium bursaria Chlorella virus 1 (PBCV-1)
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93065201; PubMed=1437552;
 RA Zhang Y., Nelson M., Nietfeld J.W., Burbank D.E., van Etten J.L.;
 RT "Characterization of Chlorella virus PBCV-1 CviA11 restriction and
 RT modification system."
 RT Nucleic Acids Res. 20:5351-5356(1992).
 RN [2]
 RP REVISIONS, AND SEQUENCE FROM N.A.
 RX MEDLINE=95133167; PubMed=7831789;
 RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., van Etten J.L.;
 RT "Analysis of 45 kb of DNA located at the left end of the Chlorella
 RT virus PBCV-1 genome."
 RT Virology 206:339-352(1995).

